


```

1 Patient No. 5970455
2 GENERAL INFORMATION:
3 APPLICANT: HITOMI, JIRO
4 APPLICANT: YAMAGUCHI, KEN
5 APPLICANT: YAMAGUCHI, KEN
6 APPLICANT: KIMURA, TATSUO
7 TITLE OF INVENTION: NOVEL CALCIUM BINDING PROTEINS
8 NUMBER OF SEQUENCES: 20
9 CORRESPONDENCE ADDRESS:
10 ADDRESS: WYAT, GERRIE, MILLER & COMPANY
11 STREET: 99 PARK AVENUE
12 STREET: 64th FLOOR
13 CITY: NEW YORK CITY
14 STATE: NEW YORK
15 COUNTRY: USA
16 ZIP: 10016
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: DISKETTE, 4.50 INCH, 720 KB
19 MEDIUM TYPE: STORAGE
20 MEDIUM TYPE: 100 PC COMPATIBLE
21 OPERATING SYSTEM: PC DOS 6.2
22 SOFTWARE: WORDPERFECT 6.1
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: 09/568,410
25 FILING DATE: DECEMBER 02, 1995
26 CLASSIFICATION: 415
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 7,704,008 AND 7,456,404 (both Japan)
29 FILING DATE: 03/12/94 AND 01/27/95, respectively
30 ATTORNEY/AGENT INFORMATION:
31 NAME: KLEIN, MILTON
32 REGISTRATION NUMBER: 27101
33 REFERENCE/WORK NUMBER: 4416
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (212)953,4450
36 TELEFAX: (212)953,4452
37 INFORMATION FOR SEQ ID NO: 19:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 92
40 TYPE: amino acid
41 STRANDNESS:
42 POSITIVITY: 100pc
43 MEDIUM TYPE: CINA
44 INFORMATION INFORMATION:
45 RELEVANT RESIDUES IN SEQ ID NO: 19:
46 FROM 1 TO 92
47 US 09 646 651a-1
48
49 Query Match: 76.2% Score 459; 106.4; Length 92;
50 Total Local Similarity: 79.1%; Total No. 7,900,482;
51 Matches: 72; Conservative: 92; Mismatches: 10; Gaps: 0;
52
53 1. EEEEEEEINHHSSVSDVAVDILKRRVYILKLNQKIKQITLSTYNI 6
54 2. EEEEEEEINHHSSVSDVAVDILKRRVYILKLNQKIKQITLSTYNI 6
55 61. DANDGVSKRVVAVVIVAHNRKE 91
56 62. DAKRCAVSEVVEVAVVAVKRAIDRIKE 92
57
58 RESULT 4
59 US 09 646 651a-1
60 Sequence 19, Application 09 US/0970455
61 Patent No. 641267
62 GENERAL INFORMATION:
63 APPLICANT: HITOMI, JIRO
64 APPLICANT: YAMAGUCHI, KEN
65 APPLICANT: YAMAGUCHI, KEN
66 APPLICANT: KIMURA, TATSUO
67 TITLE OF INVENTION: NOVEL CALCIUM BINDING PROTEINS
68 NUMBER OF SEQUENCES: 20
69 CORRESPONDENCE ADDRESS:
70 ADDRESS: WYAT, GERRIE, MILLER & COMPANY
71 STREET: 99 PARK AVENUE
72 STREET: 64th FLOOR
73 CITY: NEW YORK CITY
74 STATE: NEW YORK
75 COUNTRY: USA
76 ZIP: 10016
77 COMPUTER READABLE FORM:
78 MEDIUM TYPE: DISKETTE, 4.50 INCH, 720 KB
79 MEDIUM TYPE: STORAGE

```

```

1 ADDRESS: WYAT, GERRIE, MILLER & COMPANY
2 STREET: 99 PARK AVENUE
3 STREET: 64th FLOOR
4 CITY: NEW YORK CITY
5 STATE: NEW YORK
6 COUNTRY: USA
7 ZIP: 10016
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: DISKETTE, 4.50 INCH, 720 KB
10 MEDIUM TYPE: STORAGE
11 MEDIUM TYPE: 100 PC COMPATIBLE
12 OPERATING SYSTEM: PC DOS 6.2
13 SOFTWARE: WORDPERFECT 6.1
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: 09/568,410
16 FILING DATE: 02/29/2004, 455
17 CLASSIFICATION: 415
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 09/568,410
20 FILING DATE:
21 ATTORNEY/AGENT INFORMATION:
22 NAME: KLEIN, MILTON
23 REGISTRATION NUMBER: 27101
24 REFERENCE/WORK NUMBER: 4416
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (212)953,4450
27 TELEFAX: (212)953,4452
28 INFORMATION FOR SEQ ID NO: 19:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 92
31 TYPE: amino acid
32 STRANDNESS:
33 POSITIVITY: 100pc
34 MEDIUM TYPE: CINA
35 INFORMATION INFORMATION:
36 RELEVANT RESIDUES IN SEQ ID NO: 19:
37 FROM 1 TO 92
38 US 09 646 651a-1
39
40 Query Match: 76.2% Score 459; 106.4; Length 92;
41 Total Local Similarity: 79.1%; Total No. 7,900,482;
42 Matches: 72; Conservative: 92; Mismatches: 10; Gaps: 0;
43
44 1. EEEEEEEINHHSSVSDVAVDILKRRVYILKLNQKIKQITLSTYNI 6
45 2. EEEEEEEINHHSSVSDVAVDILKRRVYILKLNQKIKQITLSTYNI 6
46 61. DANDGVSKRVVAVVIVAHNRKE 91
47 62. DAKRCAVSEVVEVAVVAVKRAIDRIKE 92
48
49 RESULT 4
50 US 09 646 651a-1
51 Sequence 20, Application 09 US/09568410
52 Patent No. 5976842
53 GENERAL INFORMATION:
54 APPLICANT: HITOMI, JIRO
55 APPLICANT: YAMAGUCHI, KEN
56 APPLICANT: YAMAGUCHI, KEN
57 APPLICANT: KIMURA, TATSUO
58 TITLE OF INVENTION: NOVEL CALCIUM BINDING PROTEINS
59 NUMBER OF SEQUENCES: 20
60 CORRESPONDENCE ADDRESS:
61 ADDRESS: WYAT, GERRIE, MILLER & COMPANY
62 STREET: 99 PARK AVENUE
63 STREET: 64th FLOOR
64 CITY: NEW YORK CITY
65 STATE: NEW YORK
66 COUNTRY: USA
67 ZIP: 10016
68 COMPUTER READABLE FORM:
69 MEDIUM TYPE: DISKETTE, 4.50 INCH, 720 KB
70 MEDIUM TYPE: STORAGE

```

COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: MS-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US0095694 3100
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95 respectively
ATTOENEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DECKET NUMBER: 8316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: sRNA
PUBLICATION INFORMATION:
RELEVANT FEATURES IN SEQ ID NO: 20
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92

Db 59 DINSOAINFEFFIAVAKVASHKISHKE 89

RESULT 14

US-09-051-589-1

Sequence 1, Application US/09051589

Patent No. 5946080

GENERAL INFORMATION:

APPLICANT: HAGLID, Kenneth G.

TITLE OF INVENTION: USE OF PROTEIN S-100B IN MEDICINES CONTAINING THE

TITLE OF INVENTION: PROTEIN S-100B

FILE REFERENCE: 003300-478

CURRENT APPLICATION NUMBER: US/09/051,589

EARLIER FILING DATE: 1998-04-15

EARLIER APPLICATION NUMBER: SE 9503620-8

EARLIER FILING DATE: 1995-10-17

EARLIER APPLICATION NUMBER: PT/SP96/201405

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patent V2.2

SEQ ID NO: 1

LENGTH: 92

TYPE: PRO

ORGANISM: Protein S-100b

US-09-051-589-1

Query Match 33.1% Score 156 PD 2 Length 92

Best Local Similarity 37.4% Pct. No. 2.0e12

Matches 34: Conservative 17: Mismatches 40: Indels 0: Caps 0:

QY 1 TELHPEPTINPIQSVRLCHVYITIKPEKYLITKELPNIKTKRQJHUKITVNL 60

Db 2 SELEKAVALLIVIRQYSGFQDFGRKIKKSLIKLLINLSLHIFRITVAVKMETL 61

QY 61 IANMEQVSEFEVVLVTVDVLTADNHIKE 91

Db 62 DEMQDGHQDFQFMFVAMVLTACHFEFEHE 92

RESULT 15

US-07-987-272A-11

Sequence 11, Application US/07987272A

Patent No. 5731166

GENERAL INFORMATION:

APPLICANT: GREGG, C. James, R. J. and L. Kearn, H

TITLE OF INVENTION: No. 5731166-1 Chemolactic Factor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cushman Jaray & Cushman

STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower

CITY: Washington

STATE: D. C.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 435

FILING DATE: 05-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK 2127

FILING DATE: 05-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK 4463

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: Brickman, David W

REGISTRATION NUMBER: 20,817

PERFORMANCE INFORMATION: 100% 100% 100%

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861 4000

TELEFAX: 202-822 0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-987-272A-11

Query Match 33.1% Score 154 PD 1 Length 91

Best Local Similarity 37.4% Pct. No. 3.9e-12

Matches 34: Conservative 16: Mismatches 41: Indels 0: Caps 0:

QY 1 TELHPEPTINPIQSVRLCHVYITIKPEKYLITKELPNIKTKRQJHUKITVNL 60

Db 2 SELEKAVALLIVIRQYSGFQDFGRKIKKSLIKLLINLSLHIFRITVAVKMETL 61

QY 61 IANMEQVSEFEVVLVTVDVLTADNHIKE 91

Db 61 IANMEQVSEFEVVLVTVDVLTADNHIKE 91

Db 62 DEMQDGHQDFQFMFVAMVLTACHFEFEHE 91

Search completed: May 15, 2003, 11:26:43

Job time: 15 secs



1

2

3

4

GenCore version 5.1.4-F-473
Copyright (c) 1993 - 2003 GenCore Inc.

OM protein - protein search, using sw model

Run on: May 15, 2003, 11:44:19 : Search time 322 seconds

(without alignment)
176,713 million cells processed

Title: US-09-646-651A-1

Perfect score: 471

Sequence: 1 TRPROMPTINRHSVP

Scoring table: BLASTM62

Gap: 10 0 : Expect 0.5

Search: 456934 seqs, 64473310 residues

Total number of hits satisfying chosen parameters: 456934

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database	Accession	Score	Match length	DB ID	Description
1	US-09-646-651A-1	471	100	1	US-09-646-651A-1
2	US-09-646-651A-1	471	100	2	US-09-646-651A-1
3	US-09-646-651A-1	471	100	3	US-09-646-651A-1
4	US-09-646-651A-1	471	100	4	US-09-646-651A-1
5	US-09-646-651A-1	471	100	5	US-09-646-651A-1
6	US-09-646-651A-1	471	100	6	US-09-646-651A-1
7	US-09-646-651A-1	471	100	7	US-09-646-651A-1
8	US-09-646-651A-1	471	100	8	US-09-646-651A-1
9	US-09-646-651A-1	471	100	9	US-09-646-651A-1
10	US-09-646-651A-1	471	100	10	US-09-646-651A-1
11	US-09-646-651A-1	471	100	11	US-09-646-651A-1
12	US-09-646-651A-1	471	100	12	US-09-646-651A-1
13	US-09-646-651A-1	471	100	13	US-09-646-651A-1
14	US-09-646-651A-1	471	100	14	US-09-646-651A-1
15	US-09-646-651A-1	471	100	15	US-09-646-651A-1
16	US-09-646-651A-1	471	100	16	US-09-646-651A-1
17	US-09-646-651A-1	471	100	17	US-09-646-651A-1
18	US-09-646-651A-1	471	100	18	US-09-646-651A-1
19	US-09-646-651A-1	471	100	19	US-09-646-651A-1
20	US-09-646-651A-1	471	100	20	US-09-646-651A-1
21	US-09-646-651A-1	471	100	21	US-09-646-651A-1
22	US-09-646-651A-1	471	100	22	US-09-646-651A-1
23	US-09-646-651A-1	471	100	23	US-09-646-651A-1
24	US-09-646-651A-1	471	100	24	US-09-646-651A-1
25	US-09-646-651A-1	471	100	25	US-09-646-651A-1
26	US-09-646-651A-1	471	100	26	US-09-646-651A-1
27	US-09-646-651A-1	471	100	27	US-09-646-651A-1
28	US-09-646-651A-1	471	100	28	US-09-646-651A-1
29	US-09-646-651A-1	471	100	29	US-09-646-651A-1
30	US-09-646-651A-1	471	100	30	US-09-646-651A-1
31	US-09-646-651A-1	471	100	31	US-09-646-651A-1
32	US-09-646-651A-1	471	100	32	US-09-646-651A-1
33	US-09-646-651A-1	471	100	33	US-09-646-651A-1
34	US-09-646-651A-1	471	100	34	US-09-646-651A-1
35	US-09-646-651A-1	471	100	35	US-09-646-651A-1
36	US-09-646-651A-1	471	100	36	US-09-646-651A-1
37	US-09-646-651A-1	471	100	37	US-09-646-651A-1
38	US-09-646-651A-1	471	100	38	US-09-646-651A-1
39	US-09-646-651A-1	471	100	39	US-09-646-651A-1
40	US-09-646-651A-1	471	100	40	US-09-646-651A-1
41	US-09-646-651A-1	471	100	41	US-09-646-651A-1
42	US-09-646-651A-1	471	100	42	US-09-646-651A-1
43	US-09-646-651A-1	471	100	43	US-09-646-651A-1
44	US-09-646-651A-1	471	100	44	US-09-646-651A-1
45	US-09-646-651A-1	471	100	45	US-09-646-651A-1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7	354	75.2	90	15	US-09-167-705-1	Sequence 3, Appl 1
8	354	75.2	90	16	US-09-263-412-1	Sequence 3, Appl 1
9	354	75.2	90	22	US-09-826-589-3	Sequence 3, Appl 1
10	354	75.2	90	22	US-09-826-589-4	Sequence 4, Appl 1
11	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
12	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
13	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
14	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
15	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
16	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
17	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
18	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
19	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
20	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
21	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
22	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
23	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
24	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
25	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
26	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
27	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
28	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
29	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
30	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
31	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
32	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
33	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
34	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
35	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
36	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
37	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
38	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
39	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
40	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
41	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
42	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
43	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1
44	354	75.2	90	22	US-09-826-185-12	Sequence 12, Appl 1
45	354	75.2	90	22	US-09-826-185-11	Sequence 11, Appl 1

.

.

.

db 62 LITNARKGCTSEFFIMLMARLTWASHKMH 92

RESULT 7

Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
FILE REFERENCE: D0190 NP
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: 60/337,429
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patent In version 3.1
SEQ ID NO 32
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
PRT-1532 3446; 42

Query Match 43.6% Score 205.5; DB 62 Length 114;
Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

db 60 LITNARKGCTSEFFIMLMARLTWASHKMH 90
db 66 LITNARKGCTSEFFIMLMARLTWASHKMH 96

RESULT 8

Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
FILE REFERENCE: D0190 NP
CURRENT APPLICATION NUMBER: US/7,438,279
CURRENT FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: 60/337,429
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patent In version 3.1
SEQ ID NO 32
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-308-279-12

Query Match 43.6% Score 205.5; DB 62 Length 114;
Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

db 60 LITNARKGCTSEFFIMLMARLTWASHKMH 90
db 66 LITNARKGCTSEFFIMLMARLTWASHKMH 96

RESULT 9
US-60-440-068-346
GENERAL INFORMATION:
APPLICANT: Carman, Julie
TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
FILE REFERENCE: 305-4191
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: Patent In ver. 2.1
SEQ ID NO 430
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-60-440-068-340

APPLICANT: Carman, Julie

TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
FILE REFERENCE: 305-4191
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: Patent In ver. 2.1
SEQ ID NO 430
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-60-440-068-340

Query Match 43.6% Score 205.5; DB 72 Length 114;
Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

db 60 LITNARKGCTSEFFIMLMARLTWASHKMH 90
db 66 LITNARKGCTSEFFIMLMARLTWASHKMH 96

RESULT 10

Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

GENERAL INFORMATION:
APPLICANT: Carman, Julie
TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH
FILE REFERENCE: 305-4191
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: Patent In version 2.1
SEQ ID NO 430
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-60-452-680-12619

Query Match 43.6% Score 205.5; DB 72 Length 114;
Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

db 60 LITNARKGCTSEFFIMLMARLTWASHKMH 90
db 66 LITNARKGCTSEFFIMLMARLTWASHKMH 96

RESULT 11

Best Local Similarity 45.1% Pred. No. 6,26-17;
Matches 41: Conservative 23; Mismatches 26; Indels 1; Gaps 1;

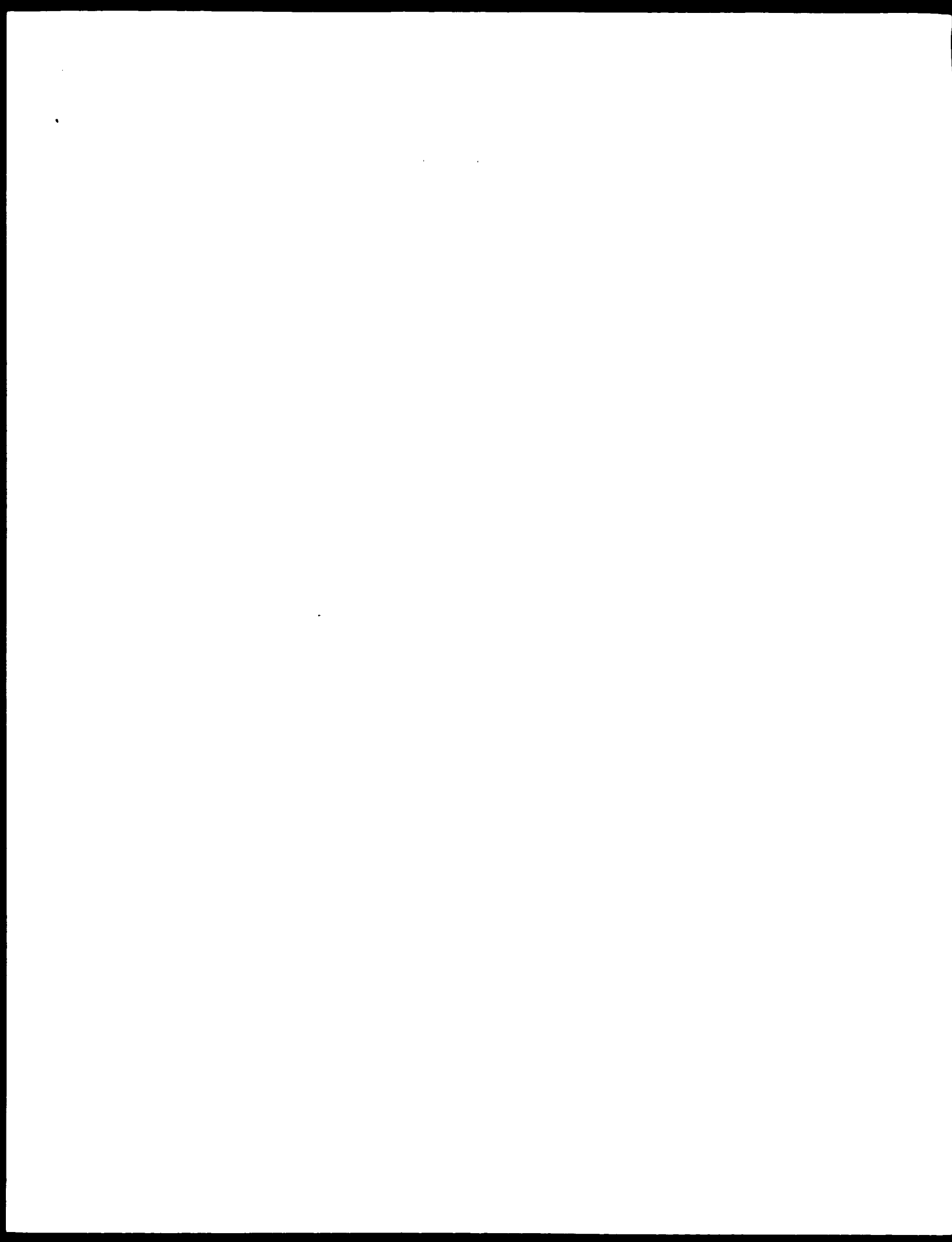
GENERAL INFORMATION:
APPLICANT: Carman, Julie
TITLE OF INVENTION: POLYPEPTIDES AND POLYPEPTIDES ASSOCIATED WITH
FILE REFERENCE: 305-4191
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: Patent In version 2.1
SEQ ID NO 430
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-60-452-680-12620

Thu May 15 11:47:29 2003

us-09-646-651a-1.rapn

Page 5

Search completed: May 15, 2003, 11:44:59
Job time : 90 secs



GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 11:34:18 : Search time 17 seconds

(without alignments)
514,602 Million cell updates/sec

Title: US-09-646-651A-1

Percent score: 471

Sequence: 1 IRTFMFGLINFRKSVV : ENVYVWVLTAMIRKE 91

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 263224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 263224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 99
Listing first 45 summaries

Database:

1: PIR1**
2: PIR2**
3: PIR3**
4: PIR4**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	455	96.6	91	2	A55406
2	399	87.9	92	1	PIR12
3	251.5	53.4	122	1	A42628
4	205.5	43.6	114	1	B11848
5	196.5	41.7	113	1	JN0686
6	179	48.0	95	2	S4146
7	168.5	45.8	113	1	S68242
8	163	44.6	95	1	S35985
9	157	44.3	89	1	S16163
10	157	44.3	101	2	S06207
11	156	43.1	92	1	A26557
12	155	42.9	91	1	B61018
13	155	42.9	92	2	A48015
14	154	42.7	92	1	BCH018
15	154	42.7	94	1	BCH01A
16	154	42.7	101	2	S01759
17	154	42.5	89	1	S09785
18	153	42.5	94	1	BCH01A
19	150	41.8	101	2	A48219
20	149	41.6	102	1	J01300
21	147	41.2	100	2	A53217
22	145	40.8	93	1	BCH030
23	145	40.8	105	1	B37680
24	144	40.6	591	2	A45145
25	143	40.4	98	2	A41988
26	140	39.7	306	2	A48118
27	136.5	29.0	110	2	B48219
28	134.5	29.6	79	1	JN0246
29	134.5	28.3	97	2	A28489

ALIGNMENTS

RESULT 1

A55406

calciumin c - pig

C13601: Sus scrofa domestica (domestic pig)

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

C13601: 10 Feb 1995 480 protein: 10 Feb 1995 #ext-change 27-May-1997

Keywords: acetylated amino acid; calcium binding; EF hand; host; amino acid; immunology

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

Accession: 277-14672

C: Superfamily; S-100 protein; calmodulin repeat homology
C: Keywords: blocked amino end, brain, calcium binding
C: Keywords: blocked amino end, brain, calcium binding

Key words: blocked amino end; brain; calcium binding; ER hand; zinc
F12-94/Product: 5-100 protein alpha chain #status produced cMAT

F: 7-41/Domain: calmodulin repeat homology <EPI>
E: 50-82/Domain: calmodulin repeat homology <IT2>

F2/Modified site, blocked amino end (Gly) (in mM)

F1, F2, F3, F4, F5, F6, F7, F8, F9, F10, F11, F12, F13, F14, F15, F16, F17, F18, F19, F20, F21, F22, F23, F24, F25, F26, F27, F28, F29, F30, F31, F32, F33, F34, F35, F36, F37, F38, F39, F40, F41, F42, F43, F44, F45, F46, F47, F48, F49, F50, F51, F52, F53, F54, F55, F56, F57, F58, F59, F60, F61, F62, F63, F64, F65, F66, F67, F68, F69, F70, F71, F72, F73, F74, F75, F76, F77, F78, F79, F80, F81, F82, F83, F84, F85, F86, F87, F88, F89, F90, F91, F92, F93, F94, F95, F96, F97, F98, F99, F100	binding site	calcium (Ser, Glu, Asp, Tyr, Gln)	status predicted
F1, F2, F3, F4, F5, F6, F7, F8, F9, F10, F11, F12, F13, F14, F15, F16, F17, F18, F19, F20, F21, F22, F23, F24, F25, F26, F27, F28, F29, F30, F31, F32, F33, F34, F35, F36, F37, F38, F39, F40, F41, F42, F43, F44, F45, F46, F47, F48, F49, F50, F51, F52, F53, F54, F55, F56, F57, F58, F59, F60, F61, F62, F63, F64, F65, F66, F67, F68, F69, F70, F71, F72, F73, F74, F75, F76, F77, F78, F79, F80, F81, F82, F83, F84, F85, F86, F87, F88, F89, F90, F91, F92, F93, F94, F95, F96, F97, F98, F99, F100	calcium (Asp, Asn, Asp, Gln, Gln)	status predicted	

Query Match 32.73; Score 154; DB 1; Length 94;

Best Local Similarity: 38.48; Pred. No. 4.1e-08;
Matches: 34; Conservative: 18; Mismatches: 35; Totals: 768

	Conservation	Misadventures	Models	Coats
1. TELEPHONE INTERVIEW EFFECTIVE TELEPHONE FOLLOW-UP FOR	10%	30%	70%	10%

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

3 SEITEAMFELINVAHASTKOGUVALEHTIELLESTILIAKAVI ANNET 62

61 | 1AN0H0VSKF9VLVTDL11AHD 86
| | | | | : : : : :
| | | | | : : : : :

FD 63 IENDDEVLIGEEVVLVAALTVACNN 88

Starch content: May 15 2003: 11.34.44

Search completed: May 15, 2003, 11:31:44
Job time : 18 secs

.

.

.

.

GmCore version 5.1.4_p5_4573
 Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

May 15, 2003, 11:24:19, 503201, 110.500045

314.52 Military - Infantry

Title: US-9-646-651A 1

Sequence: 1 TKLEDHLEIINIFHYSVR...REVVLVTVLLAANN.HHR.91

Scoring table: BIOSUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Listing first 45 summaries

Database : - SwissProt_40:*

Database : - SwissProt_40:★

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Exact Match
Re.							
1	45	96.6	91	1	S112_PIG	P1031_mus_sapien	100%
2	45	76.2	51	1	S112_B_VIR	P1731_mus_sapien	100%
3	320	67.9	91	1	S112_HUMAN	P08541_homo_sapien	100%
4	266	67.9	81	1	S112_PAFIT	P07727_cory_dactyl	100%
5	253.5	53.8	122	1	S109_BOVIN	P28731_mus_sapien	100%
6	218	43.3	119	1	M126_CHICK	P28731_mus_sapien	100%
7	206.5	43.8	118	1	S109_PAB1	P50117_cory_dactyl	100%
8	205.5	43.6	114	1	S109_HUMAN	P08722_homo_sapien	100%
9	196.5	41.7	112	1	S109_RAT	P50117_cory_dactyl	100%
10	179	38.0	95	1	S108_HUMAN	P28731_mus_sapien	100%
11	168.5	38.8	112	1	S107_MOUSE	P31722_mus_sapien	100%
12	160	34.0	92	1	S104_P1319	O10101_cory_dactyl	100%
13	159	34.8	98	1	S102_HUMAN	P08541_homo_sapien	100%
14	157	33.3	88	1	S108_MOUSE	P27055_mus_sapien	100%
15	157	33.3	88	1	S108_RAT	P50117_cory_dactyl	100%
16	157	33.3	93	1	S109_RAT	P31722_mus_sapien	100%
17	157	33.3	101	1	S104_MOUSE	P07075_mus_sapien	100%
18	156	33.1	91	1	S103_RAT	P04641_rattus_nor	100%
19	156	33.1	93	1	S10A_MOUSE	P36563_mus_muscul	100%
20	155	32.9	91	1	S108_BOVIN	P09255_bos_taurus	100%
21	155	32.9	91	1	S108_MOUSE	P50117_cory_dactyl	100%
22	154	32.7	91	1	S108_HUMAN	P08722_homo_sapien	100%
23	154	32.7	93	1	S10A_BOVIN	P32611_bos_taurus	100%
24	154	32.7	101	1	S104_RAT	P305412_rattus_nor	100%
25	153	32.5	93	1	S10A_BOVIN	P32611_bos_taurus	100%
26	153	31.8	101	1	S104_HUMAN	P28731_mus_sapien	100%
27	149	31.6	102	1	S111_PAFIT	P07727_cory_dactyl	100%
28	147	31.2	100	1	S104_BOVIN	P32611_bos_taurus	100%
29	145	30.8	93	1	S108_HUMAN	P08722_homo_sapien	100%
30	145	30.8	105	1	S111_HUMAN	P31722_mus_sapien	100%
31	143	30.4	101	1	S111_CHICK	P24472_cory_dactyl	100%
32	141	29.7	98	1	S111_MOUSE	P305412_mus_muscul	100%
33	140	29.7	93	1	S105_MOUSE	P08722_homo_sapien	100%

ALJUMMENIS

41	138	29.2	97	1	5102_HUMAN	129934	fat1a	fat1a
42	146.5	29.0	92	1	5105_HUMAN	129937	fat1b	fat1b
43	135.5	28.9	101	1	5107_HUMAN	129940	fat1c	fat1c
47	144.5	28.6	78	1	5100_HUMAN	129837	fat2	fat2
48	132.5	28.2	96	1	5110_MOUSE	129877	fat3	fat3
49	133.5	28.3	98	1	5113_HUMAN	129856	fat4	fat4
40	133	29.2	97	1	5102_HUMAN	129934	fat1a	fat1a
41	132.2	28.1	78	1	5102_HUMAN	129934	fat1a	fat1a
42	132.5	28.1	94	1	5110_MOUSE	129877	fat3	fat3
43	132	28.5	78	1	5105_HUMAN	129937	fat1b	fat1b
44	132	28.0	99	1	5111_PIG	129946	fat1d	fat1d
45	129.5	27.5	96	1	5110_CHICK	129936	fat1e	fat1e

MISSISSIPPI

ID	__S112_P10	STANDARD:	PR1:	91 AA.
07	PRO03109			
01	01-FEB-1994 (Ref.: 28, Created)			
02	01-FEB-1994 (Ref.: 28, Last sequence update)			
03	14-OCT-2001 (Ref.: 49, Last annotation update)			
DE	Calgranulin C (CASC).			
GN	S100A12.			
05	Sus scrofa (Pig).			
06	Ekkaoyota; Meluozas; Chordata; Chordata; Vertebrata; Euteleostomi;			
07	Romundia; Euthera; euteleostomi; Actinopterygii; Silur; Silur; Silur; Silur;			
08	Nhl_taxID=9824;			
09	11			
10	SEQUENCE:			
11	1153E-Granulocyte;			
12	MEDLINE 95050708; PMID=7661855;			
13	RA DeJi Angelica F.C., Schleifer C.H., Santome J.A.:			
14	Primary structure and binding properties of calgranulin C, a novel			
15	protein with calcium binding protein from pig granulocytes.";			
16	J Biol. Chem. 269:28929-28936(1994).			
17	1 TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL			
18	AMOUNTS FOUND IN LYMPHOCYTES.			
19	1 MISCELLANEOUS: IN THE ABSENCE OF ZINC IONS AND CALCIUM IONS FOR			
20	STRUCTURE, IN THE ABSENCE OF ZINC IONS AND CALCIUM IONS FOR			
21	MOLWEIGHT.			
22	1 SIMILARITY: BELONGS TO THE S-100 FAMILY.			
23	1 SIMILARITY: CONTAINS 2 EF HAND CALCIUM BINDING DOMAINS.			
24	HSSP: PRO511; 1EBA.			
25	1 InterPro: IPR001751; Calp_S100.			
26	1 InterPro: IPR002048; Ef-hand.			
27	1 Pfam: PF000456; ethand; 1.			
28	1 Pfam: PF01023; S_100; 1.			
29	1 ProDom: PD004012; Ef-hand; 1.			
30	1 ProDom: PD003407; Calp_S100; 1.			
31	1 ProSITE: PS003018; EF HAND; FALSE_NEG.			
32	1 ProSITE: PS003033; S100_CARP; 1.			
33	1 Calcium-binding; Zinc; Metal-binding.			
34	1 CA_BIND 1 (EF HAND 1 (LOW AFFINITY) (BY SIMILARITY).			
35	1 CA_BIND 2 (EF HAND 2 (HIGH AFFINITY) (BY SIMILARITY).			
36	1 CA_BIND 3 (EF HAND 3 (HIGH AFFINITY) (BY SIMILARITY).			
37	1 CA_BIND 4 (EF HAND 4 (HIGH AFFINITY) (BY SIMILARITY).			
38	1 CA_BIND 5 (EF HAND 5 (HIGH AFFINITY) (BY SIMILARITY).			
39	1 CA_BIND 6 (EF HAND 6 (HIGH AFFINITY) (BY SIMILARITY).			
40	1 CA_BIND 7 (EF HAND 7 (HIGH AFFINITY) (BY SIMILARITY).			
41	1 CA_BIND 8 (EF HAND 8 (HIGH AFFINITY) (BY SIMILARITY).			
42	1 CA_BIND 9 (EF HAND 9 (HIGH AFFINITY) (BY SIMILARITY).			
43	1 CA_BIND 10 (EF HAND 10 (HIGH AFFINITY) (BY SIMILARITY).			
44	1 CA_BIND 11 (EF HAND 11 (HIGH AFFINITY) (BY SIMILARITY).			
45	1 CA_BIND 12 (EF HAND 12 (HIGH AFFINITY) (BY SIMILARITY).			
46	1 CA_BIND 13 (EF HAND 13 (HIGH AFFINITY) (BY SIMILARITY).			
47	1 CA_BIND 14 (EF HAND 14 (HIGH AFFINITY) (BY SIMILARITY).			
48	1 CA_BIND 15 (EF HAND 15 (HIGH AFFINITY) (BY SIMILARITY).			
49	1 CA_BIND 16 (EF HAND 16 (HIGH AFFINITY) (BY SIMILARITY).			
50	1 CA_BIND 17 (EF HAND 17 (HIGH AFFINITY) (BY SIMILARITY).			
51	1 CA_BIND 18 (EF HAND 18 (HIGH AFFINITY) (BY SIMILARITY).			
52	1 CA_BIND 19 (EF HAND 19 (HIGH AFFINITY) (BY SIMILARITY).			
53	1 CA_BIND 20 (EF HAND 20 (HIGH AFFINITY) (BY SIMILARITY).			
54	1 CA_BIND 21 (EF HAND 21 (HIGH AFFINITY) (BY SIMILARITY).			
55	1 CA_BIND 22 (EF HAND 22 (HIGH AFFINITY) (BY SIMILARITY).			
56	1 CA_BIND 23 (EF HAND 23 (HIGH AFFINITY) (BY SIMILARITY).			
57	1 CA_BIND 24 (EF HAND 24 (HIGH AFFINITY) (BY SIMILARITY).			
58	1 CA_BIND 25 (EF HAND 25 (HIGH AFFINITY) (BY SIMILARITY).			
59	1 CA_BIND 26 (EF HAND 26 (HIGH AFFINITY) (BY SIMILARITY).			
60	1 CA_BIND 27 (EF HAND 27 (HIGH AFFINITY) (BY SIMILARITY).			
61	1 CA_BIND 28 (EF HAND 28 (HIGH AFFINITY) (BY SIMILARITY).			
62	1 CA_BIND 29 (EF HAND 29 (HIGH AFFINITY) (BY SIMILARITY).			
63	1 CA_BIND 30 (EF HAND 30 (HIGH AFFINITY) (BY SIMILARITY).			
64	1 CA_BIND 31 (EF HAND 31 (HIGH AFFINITY) (BY SIMILARITY).			
65	1 CA_BIND 32 (EF HAND 32 (HIGH AFFINITY) (BY SIMILARITY).			
66	1 CA_BIND 33 (EF HAND 33 (HIGH AFFINITY) (BY SIMILARITY).			
67	1 CA_BIND 34 (EF HAND 34 (HIGH AFFINITY) (BY SIMILARITY).			
68	1 CA_BIND 35 (EF HAND 35 (HIGH AFFINITY) (BY SIMILARITY).			
69	1 CA_BIND 36 (EF HAND 36 (HIGH AFFINITY) (BY SIMILARITY).			
70	1 CA_BIND 37 (EF HAND 37 (HIGH AFFINITY) (BY SIMILARITY).			
71	1 CA_BIND 38 (EF HAND 38 (HIGH AFFINITY) (BY SIMILARITY).			
72	1 CA_BIND 39 (EF HAND 39 (HIGH AFFINITY) (BY SIMILARITY).			
73	1 CA_BIND 40 (EF HAND 40 (HIGH AFFINITY) (BY SIMILARITY).			
74	1 CA_BIND 41 (EF HAND 41 (HIGH AFFINITY) (BY SIMILARITY).			
75	1 CA_BIND 42 (EF HAND 42 (HIGH AFFINITY) (BY SIMILARITY).			
76	1 CA_BIND 43 (EF HAND 43 (HIGH AFFINITY) (BY SIMILARITY).			
77	1 CA_BIND 44 (EF HAND 44 (HIGH AFFINITY) (BY SIMILARITY).			
78	1 CA_BIND 45 (EF HAND 45 (HIGH AFFINITY) (BY SIMILARITY).			
79	1 CA_BIND 46 (EF HAND 46 (HIGH AFFINITY) (BY SIMILARITY).			
80	1 CA_BIND 47 (EF HAND 47 (HIGH AFFINITY) (BY SIMILARITY).			
81	1 CA_BIND 48 (EF HAND 48 (HIGH AFFINITY) (BY SIMILARITY).			
82	1 CA_BIND 49 (EF HAND 49 (HIGH AFFINITY) (BY SIMILARITY).			
83	1 CA_BIND 50 (EF HAND 50 (HIGH AFFINITY) (BY SIMILARITY).			
84	1 CA_BIND 51 (EF HAND 51 (HIGH AFFINITY) (BY SIMILARITY).			
85	1 CA_BIND 52 (EF HAND 52 (HIGH AFFINITY) (BY SIMILARITY).			
86	1 CA_BIND 53 (EF HAND 53 (HIGH AFFINITY) (BY SIMILARITY).			
87	1 CA_BIND 54 (EF HAND 54 (HIGH AFFINITY) (BY SIMILARITY).			
88	1 CA_BIND 55 (EF HAND 55 (HIGH AFFINITY) (BY SIMILARITY).			
89	1 CA_BIND 56 (EF HAND 56 (HIGH AFFINITY) (BY SIMILARITY).			
90	1 CA_BIND 57 (EF HAND 57 (HIGH AFFINITY) (BY SIMILARITY).			
91	1 CA_BIND 58 (EF HAND 58 (HIGH AFFINITY) (BY SIMILARITY).			
92	1 CA_BIND 59 (EF HAND 59 (HIGH AFFINITY) (BY SIMILARITY).			
93	1 CA_BIND 60 (EF HAND 60 (HIGH AFFINITY) (BY SIMILARITY).			
94	1 CA_BIND 61 (EF HAND 61 (HIGH AFFINITY) (BY SIMILARITY).			
95	1 CA_BIND 62 (EF HAND 62 (HIGH AFFINITY) (BY SIMILARITY).			
96	1 CA_BIND 63 (EF HAND 63 (HIGH AFFINITY) (BY SIMILARITY).			
97	1 CA_BIND 64 (EF HAND 64 (HIGH AFFINITY) (BY SIMILARITY).			
98	1 CA_BIND 65 (EF HAND 65 (HIGH AFFINITY) (BY SIMILARITY).			
99	1 CA_BIND 66 (EF HAND 66 (HIGH AFFINITY) (BY SIMILARITY).			
100	1 CA_BIND 67 (EF HAND 67 (HIGH AFFINITY) (BY SIMILARITY).			

[illegible]

1 TISSUE SPECIFICITY: FOUND ESSENTIALLY IN EPIDERMAL TISSUES.
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000

